

SEQUENCE LISTING

SEQ ID NO: 1 - SARS Coronavirus Urbani S-protein full-length gene sequence (AY278741, 3768 bps)

atgtttattttctattatttctactctactagtggtagtgaccttgaccgggtgcaccacttttgatgatgttcaagctcc
taattacactcaacatacttcatctatgaggggggttactatcctgatgaaatttttagatcagacactctttatttaactcag
gattatttctccattttatttctaattgttacagggttcatactattaatcatacgtttggcaaccctgtcatacctttaaggat
ggtattttttgctgccacagagaaatcaaatgttgccgtggttgggttttgggttctacatgaacaacaagtcacagtc
ggtgattattattaacaatttactaatgttggtatagcagcatgaacttgaattgttgacaacccttcttctgctgttctaa
acccatgggtacacagacacatactatgatattcgataatgcatttaattgcacttctgagtacatatctgatgccttttcgc
ttgatgttccagaaaagtcaggtaattttaacacttacgagagtttgtgtttaaaaataaagatgggttctctatgtttataa
gggctatcaacctatagatgtagttcgtgatctaccttctggttttaacactttgaaacctattttaagttgcctcttggtatta
acattacaaatttttagagccattcttacagcctttcacctgctcaagacatttggggcacgtcagctgcagcctattttgtt
ggctatttaaagccaactacatttatgctcaagtatgatgaaatggtacaatcacagatgctgttgattgttctcaaaatcc
acttgcgtgaactcaaatgctctgttaagagctttgagattgacaaaggaatttaccagaccttaatttcagggttgttccct
caggagatgttgtagattccctaataattacaaactgtgtcctttggagaggttttaattgctactaaattcccttctgtcta
tgcatgggagagaaaaaaatttctaattgtgtgctgattactctgtgctctacaactcaacattttttcacctttaagt
ctatggcgtttctgccactaagttgaatgatctttgcttctccaatgtctatgcagattcttttagtcaaggaggatgatgt
aagacaaatagcgccaggacaaactggtgtattgctgattataattataaattgccagatgattcatgggtgtgtcctt
gcttggaaactaggaacattgatgctacttcaactggtaattataaattataaattataggtatcttagacatggcaagcttag
gccctttgagagagacatatctaattgtgcctttctcccctgatggcaaaccttgcacccacctgctcttaattgttattggc
cattaaatgattatggtttttacaccactactggcattggctaccaaccttacagagttgtagtacttctttgaacttttaaat
gcaccggccacggtttgtggacaaaattatccactgaccttattaagaaccagtgtgtcaattttaatttaattggaactca
ctggtactggtgtgttaactccttctcaaagagatttcaaccatttcaacaatttggccgtgatgttctgatttactgattc
cgttcgagatcctaaaacatctgaaatattagacatttcccttgccttttgggggtgtaagtgaattacacctggaaca
aatgcttcatctgaagtgtgtgtctatatcaagatgttaactgcactgatgtttctacagcaattcatgcagatcaactcac
accagcttggcgcatatatttacttgaaacaatgtattccagactcaagcaggctgtcttataggagctgagcatgtcg
acacttcttatgagtgcgacattcctattggagctggcattgtgtgctagtaccatacagttctttattacgtagtactagcc
aaaaatctatttggcttatactatgtcttttaggtgctgatagttcaattgcttacttataaacaccattgctatacctactaa
cttttaattagcattactacagaagtaattgcctgtttctatgggttaaaacctccgtagattgtaatatgtacatctgcggag
atttactgaattgtgctaatttgccttccaatatggtagcttttgcacacaactaaatcgtgcactctcaggtattgtctgtg
aacaggatcgcaacacacgtgaagtgttcgctcaagtcaacaatgtacaaaaccccaacttgaataatttgggtgtg
tttaattttcacaaatattacctgaccttctaaagccaactaagaggtcttttattgaggactgtctttaaataaggtgaca
ctcgtgatgctggcttcatgaagcaatatggcgaatgcttaggtgatattaatgctagagatctcatttgcgcgagaag
ttcaatggacttacagtgttggcacctctgctcactgatgatgattgctgcctacactgctgctctagttagtggtactgc
cactgctggatggacatttgggtgctggcgtgctcttcaaataccttttgcctatgcaaatggcatataggttcaatggcatt
ggagttacccaaaatgttctctatgagaacaaaaacaaatcgccaaccaatttaacaaggcgattagtcaaattcaaga
atcattacaacaacatcaactgcattgggcaagctgcaagacgttgttaaccagaatgtcaagcattaaacacacttg
ttaaacaacttagctctaatttgggtgcaatttcaagtgtgctaatgatattcctttcgcgacttgataaagtcgaggcggag
gtacaaattgacagggttaattacaggcagacttcaaagccttcaaacctatgtaacacaacaactaatcagggtgctga
aatcagggtcttctgctaatttgcgtgctactaaaatgtctgagtgtgttcttggacaatcaaaaagagttgacttttggaa
agggtaccaccttatgtccttcccacaagcagccccgatggtgtgtcttctacatgtcacgtatgtgccatcccag
gagaggaacttaccacagcgccagcaatttgcataaggaagcatacttccctcgtgaaggtgttttgtgtttaat
ggcacttcttgggttattacacagaggaacttcttctccacaataattactacagacaataatttgcctcaggaaattgt
gatgtcgttattggcatcattaacaacacagtttatgacctctgcaacctgagctcgactcattcaagaagagctggac
aagtacttcaaaaatcatacatcaccagatgttgatcttggcgacatttcaggcattaacgccttctgtcgtcaacattcaaa

aagaaattgaccgcctcaatgaggtcgctaaaaatttaaatgaatcactcattgaccttcaagaattgggaaaatatgag
caatatattaaatggccttggatgtttggctcggcttcattgctggactaattgccatcgatggttacaatctgdtgtt
gcatgactagtgttgacgttgcctcaagggatgcatgctcttggttcttgctgcaagttgatgaggatgactctgagcc
agttctcaaggggtgcaaattacattacacataa

SEQ ID NO: 2 - Protein sequence for full length S-protein from accession number AAP13441 corresponding to the gene AY278741 (1256aa)

MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPDEIFRS
DTLYLTQDLFLPFYSNVTGFHTINHTFGNPVIPFKDGIYFAATEKSNVVRG
WVFGSTMNNKSQSVMNNSTNVVIRACNFELCDNPFFAVSKPMGTQTHTM
IFDNAFNCTFEYISDAFSLDVSEKSGNFKHLREFVFKNKDGFLYVYKGYQPI
DVVRDLPSGFNTLKPIFKLPLGINITNFRAILTAFSPAQDWGTSAAAAYFVG
YLKPTTFMLKYDENGITITDAVDCSQNPLAELKCSVKSFEDKGIYQTSNFR
VVPSGDVVRFPNITNLCPFGEVFNATKFPSVYAWERKKISNCVADYSVLY
NSTFFSTFKCYGVSATKLNLDLCSNVYADSFVVKGDDVRQIAPGQTGVIA
DYNKLPDDFMGCVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFERDI
SNVPFSPDGKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVVLSEFLLNA
PATVCGPKLSTDLIKNQCVNFNENGLTGTGVLTPSSKRFQPFQQFGRDVSD
FTDSVRDPKTSEILDSPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTA
IHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYH
TVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMA
KTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTREVF
AQVKQMYKTPTLK YFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTADAGF
MKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGTAT
AGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAIS
QIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRL
DKVEAEVQIDRLITGRLOSLQTYVTQQLIRAAEIRASANLAATKMSECVLG
QSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERNFTTAPAICHEG
KAYFPREGVVFVNGTSWFITQRNFFSPQIITTDNTFVSGNCDVVIGIINNTVY
DPLQPELDSFKEELDKYFKNHTSPDVDLGDISGINASVVNIQKEIDRLNEVA
KNLNEIDLQELGKYEYIKWPWYVWLGFIAGLIAIVMVTILLCCMTSCC
SCLKGACSCGSCCKFDEDDSEPVLKGVKLHYT

**SEQ ID NO: 3 - Protein sequence for Spike protein amino acid 275-1081
from accession number AAP13441 (807aa) (wild type, wt):**

AVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVVPSPGDVVRFPNITNLC
PFGEVFNATKFPSVYAWERKKISNCVADYSVLYNSTFFSTFKCYGVSATK
LNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLA
WNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVPFSPDGKPCTPPALN
CYWPLNDYGFYTTTGIGYQPYRVVVLSELLNAPATVCGPKLSTDLIKNO
CVNFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISP
CSFGGVSIVTPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGN
NVFQTQAGCLIGAEHVDTSYECDIPGAGICASYHTVSLRSTSQKSIVAYT
MSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTE
CANLLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFG
GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLI
CAQKFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAM
QMA YRFNGIGVTQNVLYENQKQLANQFNKAISQIQESLTTTSTALGKLQDV
VNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQS
LQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFP
QAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVNG

**SEQ ID NO: 4 - Protein sequence for Spike protein amino acid 275-1081
mutant with 9 potential N-linked glycosylation sites eliminated
(807aa)(substituted Alanine shown as "a")(mutant, mt):**

AVDCSQNPLAELKCSVKSFEDKGIYQTSNFRVVPSPGDVVRFPNlaNLCP
FGEVFaATKFPSVYAWERKKISNCVADYSVLYNsaFFSTFKCYGVSATKLN
DLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWN
TRNIDATSTGNYNKYRYLRHGKLRPFERDISNVPFSPDGKPCPPALNCY
WPLNDYGFYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNCV
NFnFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFDTSVRDPKTSEILDISPCS
FGGVSVITPGTNaSEVAVLYQDVaCTDVSTAIHADQLTPAWRIYSTGNNV
FQTQAGCLIGAETHVDTSYECDIPIGAGICASYHTVSLLRSTSQKSIVAYTMS
LGADSSIAYSaNTIAIPTNFaISITTEVMPVSMAKTSVDCNMYICGDSTECAN
LLLQYGSFCTQLNRALSGIAAEQDRNTREVFQAQVKQMYKTPTLKYFGGFN
FaQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQ
KFNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQM
AYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVN
QNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQ
TYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSPQA
APHGVVFLHVTYVPSQERNFaTAPAICHEGKAYFPREGVFVFNG

SEQ ID NO: 5 - The gene sequence for Spike protein amino acid 275-1081 mutant (807aa) with native virus codons and elimination of N-glycosylation sites (2421bp) (substituted nucleotides shown capitalized):

gctgttgattgttctcaaaatccacttgctgaactcaaatgctctgttaagagctttgagattgacaaaggaattacc
agacctctaatttcagggtgttcctcaggagatgttgtagattccctaattGcaaacttggtccttttgagaggtt
tttGCCgctactaaattcccttctgtctatgcatgggagagaaaaaatttctaattgtttgctgattactctgtgctcta
caactcaGcattttttcaacctttaagtgtatggcgtttctgccactaagttgaatgatctttgcttctcaatgtctatga
gattctttttagtcaaggagatgatgtaagacaaaatagcgccaggacaaaactgggttattgctgattataattataaat
tgccagatgattcatgggtgtgtccttgcttggaaactaggaacattgatgctacttcaactggtaattataattataaat
ataggtatcttagacatggcaagcttaggccctttgagagagacatatctaattgtgccttttccccctgatggcaacctt
gcacccccactgctctaattgtattggccattaaatgattatggttttacaccactactggcattggctaccaaccttaca
gagttgtagtactttttgaacttttaaatgcacgggccacgggttgggacaaaattatccactgaccttattaagaac
cagtgtgtcaattttaatttaattggactcactgggtactgggtgtgtaactccttctcaaagagattcaaccatttcaacaat
ttggccgtgatgtttctgattcactgattccgttcgagatcctaaaacatctgaaatattagacattcaccctgctcttttg
gggtgtaagtgaattacacctggaacaaatgctGcatctgaagttgctgttctatatcaagatgttGCctgactgatg
ttctacagcaattcatgcagatcaactcacaccagcttggcgcatatattctactggaaacaatgtattccagactcaag
caggctgtcttataggagctgagcatgtcgacacttcttatgagtgcgacattcctattggagctggcatttgtgctgtta
ccatacagtttcttattacgtagtagttagccaaaaatctattgtggcttatactatgtctttaggtgctgatagttcaattgctt
actctGCCaacaccattgctatacctactaactttGcaattagcattactacagaagtaatgcctgtttctatggctaaaa
cctccgtagattgtaatatgtacatctgcggagattctactgaatgtgctaattgcttctccaatatggtagctttgacac
aactaaatcgtgcactctcagggtattgctgctgaacaggatcgcaacacacgtgaagtgttcgctcaagtcaaaacaat
gtacaaaaccccaactttgaaatattttgggtggttttaattttGcacaatattacctgacctctaaagccaactaagagg
tcttttattgaggactgctctttaataagggtgacactcgtgtgctggcttcatgaagcaatatggcgaatgcctaggtg
atattaatgctagagatctcatttgtgcgcagaagttcaatggacttacagtgttgcacctctgctcactgatgatgatt
gctgcctacactgctgctctagtttagtggtactgccactgctggatggacatttgggtgctggcgtgcttctcaaatcctt
ttgctatgcaaatggcatataggttcaatggcattggagttacccaaaatgttctctatgagaacaaaaaacaatcgcca
accaatttaacaaggcgattagtc aaattcaagaatcacttacaacaacatcaactgcattgggcaagctgcaagacggtt
gttaaccagaatgctcaagcattaaacacacttgtaaacaacttagctctaattttgggtgcaatttcaagtgtgctaaatga
tatcctttcgcgacttgataaagtcgaggcggagggtacaaattgacagggttaattacaggcagacttcaagccttcaaa
cctatgtaacacaacaactaatcagggtgctgaaatcagggttctgctaattctgctgctactaaaatgtctgagtgtgt
tcttgacaatcaaaaagagttgacttttggaaagggtaccaccttatgtccttcccacaagcagccccgcatgggtg
ttgtcttctacatgtcacgtatgtgccatcccaggagagggaacttcGccacagcgccagcaatttgc atgaaggcaa
agcactactccctcgtgaagggtgttttgtgttaatggc

SEQ ID NO: 6 - The gene sequence for Spike protein amino acid 275-1081 mutant (807aa) with altered codon usage to enhance expression and elimination of N-glycosylation sites (2421bp):

GCCGTGGACTGCTCCCAGAACCCCTGGCCGAGCTGAAGTGCTCCGTGAAGT
CCTTCGAGATCGACAAGGGCATCTACCAGACCTCCAACCTCCGCGTGGTGCCCTC
CGGCGACGTGGTGCCTTCCCCAACATCGCCAACCTGTGCCCTTCGGCGAGGTG
TTCGCCGCCACCAAGTTCCTTCCGTGTACGCTGGGAGCGCAAGAAGATCTCCA
ACTGCGTGGCCGACTACTCCGTGCTGTACAACTCCGCCTTCTTCTCCACCTTCAA
GTGCTACGGCGTGTCCGCCACCAAGCTGAACGACCTGTGCTTCTCCAACGTGTAC
GCCGACTCCTTCGTGGTGAAGGGCGACGACGTGCGCCAGATCGCCCCCGGCCAGA
CCGGCGTGATCGCCGACTACAACTACAAGCTGCCCGACGACTTCATGGGCTGCGT
GCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCAACTACAATAC
AAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCCTTCGAGCGCGACATCTCCA
ACGTGCCCTTCTCCCCCGACGGCAAGCCCTGCACCCCCCGCCCTGAACTGCTA
CTGGCCCCCTGAACGACTACGGCTTCTACACCACCACCGGCATCGGCTACCAGCCC
TACCGCGTGGTGGTGTCTTCTGAGCTGCTGAACGCCCCCGCCACCGTGTGCG
GCCCCAAGCTGTCCACCGACCTGATCAAGAACCAGTGCGTGAACCTTCAACTTCAA
CGGCCTGACCGGCACCGGCGTGTGACCCCCTCCTCCAAGCGCTTCCAGCCCTTC
CAGCAGTTCGGCCGCGACGTGTCCGACTTCACCGACTCCGTGCGCGACCCCCAAGA
CCTCCGAGATCCTGGACATCTCCCCCTGCTCCTTCGGCGGCGTGTCCGTGATCAC
CCCCGGCACCAACGCCGCTCCGAGGTGGCCGTGCTGTACCAGGACGTGGCCTGC
ACCGACGTGTCCACCGCCATCCACGCCGACCAGCTGACCCCCGCTGGCGCATCT
ACTCCACCGGCAACAACGTGTTCCAGACCCAGGCCGGCTGCCTGATCGGCGCCGA
GCACGTGGACACCTCCTACGAGTGCACATCCCCATCGGCGCCGGCATCTGCGCC
TCCTACCACACCGTGTCCCTGCTGCGCTCCACCTCCCAGAAGTCCATCGTGGCCT
ACACCATGTCCCTGGGCGCCGACTCCTCCATCGCCTACTCCGCCAACACCATCGC
CATCCCCACCAACTTCGCCATCTCCATCACCACCGAGGTGATGCCCGTGTCCATG
GCCAAGACCTCCGTGGACTGCAACATGTACATCTGCGGCGACTCCACCGAGTGCG
CCAACCTGCTGCTGCAGTACGGCTCCTTCTGCACCCAGCTGAACCGCGCCCTGTC
CGGCATCGCCGCCGAGCAGGACCGCAACACCCGCGAGGTGTTGCCCCAGGTGAAG
CAGATGTACAAGACCCCCACCCTGAAGTACTTCGGCGGCTTCAACTTCGCCCAGA
TCCTGCCCGACCCCCCTGAAGCCCACCAAGCGCTCCTTCATCGAGGACCTGCTGTT
CAACAAGGTGACCCTGGCCGACGCCGGCTTCATGAAGCAGTACGGCGAGTGCCCTG
GGCGACATCAACGCCCGCGACCTGATCTGCGCCCAGAAGTTCAACGGCCTGACCG
TGCTGCCCCCCTGCTGACCGACGACATGATCGCCGCCCTACACCGCCGCCCTGGT
GTCCGGCACCGCCACCGCCGGCTGGACCTTCGGCGCCGGCGCCCTGCAGATC
CCCTTCGCCATGCAGATGGCCTACCGCTTCAACGGCATCGGCGTGACCCAGAACG
TGCTGTACGAGAACCAGAAGCAGATCGCCAACCAAGTTCAACAAGGCCATCTCCCA
GATCCAGGAGTCCCTGACCACCACCTCCACCGCCCTGGGCAAGCTGCAGGACGTG
GTGAACCAGAACGCCAGGCCCTGAACACCCTGGTGAAGCAGCTGTCTTCAACT
TCGGCGCCATCTCCTCCGTGCTGAACGACATCCTGTCCCGCCTGGACAAGGTGGA
GGCCGAGGTGCAGATCGACCGCTGATCACCAGCGCCCTGCAGTCCCTGCAGACC
TACGTGACCCAGCAGCTGATCCGCGCCGCCGAGATCCGCGCCTCCGCCAACCTGG
CCGCCACCAAGATGTCCGAGTGCGTGTGGGCCAGTCCAAGCGCGTGGACTTCTG
CGGCAAGGGCTACCACCTGATGTCTTCCCCAGGCCGCCCCCACGGCGTGGTG
TTCCTGCACGTGACCTACGTGCCCTCCAGGAGCGCAACTTCGCCACCGCCCCCG
CCATCTGCCACGAGGGCAAGGCCCTACTTCCCCCGGAGGGCGTGTTCGTGTTCAA
CGGC

SEQ ID NO: 7 - Potential N-glycosylation sites within the protein sequence of the Spike protein amino acid 275-1081 (807aa) (wild type, wt) with potential N-glycosylation sites underlined.

AVDCSQNPLAELKCSVKSF¹FEIDKGIYQTSNFRVVP²SGDVVRFPNITNLC
 PFGEVFNATKFP³SVYAWERKKISNCVADYSVL⁴YNSTFFSTFKCYGVSATK
 LNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKL⁵PDDFMGCVLA
 WNTRNIDATSTGN⁶YNYKYRYLRHGKLRP⁷FERDISNVPFSPDGK⁸PCTPPALN
 CYWPLNDYGFYTTTGIGYQPYRVV⁹VLSFELLNAPATVCGPKLSTDLIKNQ
 CVN¹⁰FNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDISP
 CSFGGVS¹¹VITPGTNA¹²SEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGN
 NVFQTQAGCLIGAEHVDTSYEC¹³DIPIGAGICASYHTVSLRSTSQKSIVAYT
 MSLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTE
 CANLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLK¹⁴YFG
 GFNFSQILPDPLKPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLI
 CAQKFNGLT¹⁵VLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAM
 QMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDV
 VNQNAQALNTLVKQLSSNFGA¹⁶ISSVLNDILSRLDKVEAEVQIDRLITGRLQS
 LQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHLMSFP
 QAAPHGVVFLHVTYVPSQERNFTTAPAICHEGKAYFPREGVVFVNG

SEQ ID NO: 8 Amino acid sequence of Region II peptide

VLYN¹SAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADY
 NYKL²PDDFMGCVLAWNTRNIDATSTGN³YNYKYRYLRHGKLRP⁴FERDISNVPFSP
 DGK⁵PCTPPALNCYWPLNDYGFYTTTGIGYQPYRVV⁶VLSFELLNAPATVCGPKLST
 DLIKNQCVN⁷FNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDIS
 PCSFGGVS⁸VITPGTNAASEVAVLYQDV

SEQ ID NO: 9 Amino acid sequence of Region III peptide

AEQDRNTREVFAQVKQMYKTPTLK¹YFGGFNFAQILPDPLKPTKRSFIEDLLFNKV
 TLADAGFMKQYGECLGDINARDLICAQKFNGLT²VLPPLLTDDMIAAYTAALVSGT
 ATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQ
 ESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGA³ISSVLNDILSRLDKVEAEV
 QIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKG
 YHL

SEQ ID NO: 10 Amino acid sequence of Region IV peptide

VLYN¹SAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADY
 NYKL²PDDFMGCVLAWNTRNIDATSTGN³YNYKYRYLRHGKLRP⁴FERDISNVPFSP
 DGK⁵PCTPPALNCYWPLNDYGFYTTTGIGYQPYRVV⁶VLSFELLNAPATVCGPKLST
 DLIKNQCVN⁷FNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILDIS
 PCSFGGVS⁸VITPGTNAASEVAVLYQDVACTDVSTAIHADQLTPAWRIYSTGNNVF

QTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSLGADSS
IAYSANTIAIPTNFASITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCT
QLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDPLKPTKRS
FIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIA
AYTAALVSGTATAGWTFGAGAALQIPFAMQMA YRFNGIGVTQNVLYENQKQIA
NQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDI
LSRLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLGQ
SKRVDFCGKGYHL

SEQ ID NO: 11 Amino acid sequence of Region II peptide from Spike protein from accession number AAP13441(wild type)

VLNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQ
TGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRP
FERDISNVPFSPDGKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVLSF
ELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFG
RDVSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDV

SEQ ID NO: 12 Amino acid sequence of Region III peptide from Spike protein from accession number AAP13441(wild type)

AEQDRNTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIED
LLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMI
AAYTAALVSGTATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYEN
QKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNF
GAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASAN
LAATKMSECVLGQSKRVDFCGKGYHL

SEQ ID NO: 13 Amino acid sequence of Region IV peptide from Spike protein from accession number AAP13441(wild type):

VLNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTG
VIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRPFE
RDISNVPFSPDGKPCTPPALNCYWPLNDYGFYTTTGIGYQPYRVVLSFEL
LNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPFQQFGRD
VSDFTDSVRDPKTSEILDISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDV
STAIHADQLTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICA
SYHTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISITTEVMPVS
MAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRALSGIAAEQDRNTRE
VFAQVKQMYKTPTLKYFGGFNFSQILPDPLKPTKRSFIEDLLFNKVTLADA
GFMKQYGECLGDINARDLICAQKFNGLTVLPPLLTDDMIAAYTAALVSGT
ATAGWTFGAGAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKA
ISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILS
RLDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECV
LGQSKRVDFCGKGYHL

SEQ ID NO: 14 Amino acid sequence of Region IV peptide from Spike protein from accession number AAP13441(wild type):

AVDCSQNPLAELKCSVKSFEDKGIYQTSNFRVVPBGDVVRFPNITNLCPFG
 EVFNATKFPSVYAWERKKISNCVADYSVLNSTFFSTFKCYGVSATKLN
 LCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNT
 RNIDATSTGNYNYKYRYLRHGKLRPFERDISNVPFSPDGKPCPPALNCY
 WPLNDYGFYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNCV
 NFNFNGLTGTGVLTPSSKRFQPFQQFGRDVSDFDTSVRDPKTSEILDSPCS
 FGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLTPAWRIYSTGNN
 VFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTM
 SLGADSSIAYSNNTIAIPTNFSISITTEVMPVSMAKTSVDCNMYICGDSTCA
 NLLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGF
 NFSQILPDPLKPTKRSFIEDLLFNKVTADAGFMKQYGECLGDINARDLCA
 QKFNGLTVLPPLLTDDMLAAYTAALVSGTATAGWTFGAGAALQIPFAMQ
 MAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVV
 NQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSL
 QTYVTQQLIRAAEIRASANLAATKMSECVLGQSKRVDFCGKGYHL

SEQ ID NO: 15 Linker for nucleotide primer oligo #1

TCGCTCGAGAAAAGAGTGCTCTACAACTCAGCATT

SEQ ID NO: 16 Linker for nucleotide primer oligo #2

ATCTCTAGATTAAACATCTTGATATAGAACAGC

SEQ ID NO: 17 Linker for nucleotide primer oligo #3 TCGCTCGAG

AAAAGAGCTGAACAGGATCGCAACACA

SEQ ID NO: 18 Linker for nucleotide primer oligo #4

ATCTCTAGATTAAAGGTGGTAGCCCTTCC

SEQ ID NO: 19 SARS Spike Glycoprotein Fragment synthetic DNA sequence with N-lined glycosylation site mutations (2421 bp)

GCCGTGGACTGCTCCCAGAACCCACTGGCCGAGCTGAAGTGCTCCGTGA
 AGTCCTTCGAGATCGACAAGGGCATCTACCAGACCTCCAACCTCCGCGTG
 GTGCCATCCGGCGACGTGGTGCGCTTCCCAAACATCGCCAACCTGTGCC

CATTCGGCGAGGTGTTTCGCCGCCACCAAGTTCCCATCCGTGTACGCCTG
GGAGCGCAAGAAGATCTCCAACCTGCGTGGCCGACTACTCCGTG
CTGTACAACTCCGCCTTCTTCTCCACCTTCAAGTGCTACGGCGTGTCCGC
CACCAAGCTGAACGACCTGTGCTTCTCCAACGTGTACGCCGACTCCTTCG
TGGTGAAGGGCGACGACGTGCGCCAGATCGCCCCAGGCCAGACCGGCGT
GATCGCCGACTACAACCTACAAGCTGCCAGACGACTTCATGGGCTGCGTG
CTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCAACTACA
ACTACAAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCCATTCGAGCG
CGACATCTCCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCACCCAC
CAGCCCTGAACTGCTACTGGCCACTGAACGACTACGGCTTCTACACCACC
ACCGGCATCGGCTACCAGCCATACCGCGTGGTGGTGCTGTCCTTCGAGC
TGCTGAACGCCCCAGCCACCGTGTGCGGCCCAAAGCTGTCCACCGACCT
GATCAAGAACCAGTGCGTGAACCTTCAACTTCAACGGCCTGACCGGCACC
GGCGTGCTGACCCCATCCTCCAAGCGCTTCCAGCCATTCCAGCAGTTCGG
CCGCGACGTGTCCGACTTCACCGACTCCGTGCGCGACCCAAAGACCT
CCGAGATCCTGGACATCTCCCCATGCTCCTTCGGCGGGCGTGTCCGTGATC
ACCCAGGCACCAACGCCGCCTCCGAGGTGGCCGTGCTGTACCAGGACG
TGGCCTGCACCGACGTGTCCACCGCCATCCACGCCGACCAGCTGACCCC
AGCCTGGCGCATCTACTCCACCGGCAACAACGTGTTCCAGACCCAGGCC
GGCTGCCTGATCGGCGCCGAGCACGTGGACACCTCCTACGAGT
GCGACATCCCAATCGGCGCCGGCATCTGCGCCTCCTACCACACCGTGTC
CCTGCTGCGCTCCACCTCCAGAAGTCCATCGTGGCCTACACCATGTCCC
TGGGCGCCGACTCCTCCATCGCCTACTCCGCCAACACCATCGCCATCCCA
ACCAACTTCGCCATCTCCATCACCACCGAGGTGATGCCAGTGTCCATGGC
CAAGACCTCCGTGGACTGCAACATGTACATCTGCGGCGACTCCACCGAG
TGCGCCAACCTGCTGCTGCAGTACGGCTCCTTCTGCACCCAGCTGAACCG
CGCCCTGTCCGGCATCGCCGCCGAGCAGGACCGCAACACCCGCGAGGTG
TTCGCCCAAGGTGAAGCAGATGTACAAGACCCCAACCCTGAAGTACTTCG
GCGGCTTCAACTTCGCCCAGATCCTGCCAGACCCACTGAAGCCAACCAA
GCGCTCCTTCATCGAGGACCTGCTGTTCAACAAGGTGACCCTGGCCGAC
GCCGGCTTCATGAAGCAGTACGGCGAGTGCCTGGGCGACATCAACGCCC
GCGACCTGATCTGCGCCCAGAAGTTCAACGGCCTGACCGTGCTGCCACC
ACTGCTGACCGACGACATGATCGCCGCCTACACCGCCGCCCTGGTGTC
CGGCACCGCCACCGCCGGCTGGACCTTCGGCGCCGGCGCCGCCCTGCAG
ATCCCATTCGCCATGCAGATGGCCTACCGCTTCAACGGCATCGGCGTGAC
CCAGAACGTGCTGTACGAGAACCAGAAGCAGATCGCCAACCAGTTCAAC
AAGGCCATCTCCCAGATCCAGGAGTCCCTGACCACCACCTCCACCGCCCT
GGGCAAGCTGCAGGACGTGGTGAACCAGAACGCCCAAGGCCCT
GAACACCCTGGTGAAGCAGCTGTCTCCAACCTTCGGCGCCATCTCCTCCG
TGCTGAACGACATCCTGTCCCGCCTGGACAAGGTGGAGGCCGAGGTGCA
GATCGACCGCCTGATCACCGGCCGCCTGCAGTCCCTGCAGACCTACGTG
ACCCAGCAGCTGATCCGCGCCGCCGAGATCCGCGCCTCCGCCAACCTGG
CCGCCACCAAGATGTCCGAGTGCGTGCTGGGCCAGTCCAAGCG
CGTGGACTTCTGCGGCAAGGGCTACCACCTGATGTCCTTCCCACAGGCC
GCCCCACACGGCGTGGTGTTCCTGCACGTGACCTACGTGCCATCCCAGG
AGCGCAACTTCGCCACCGCCCCAGCCATCTGCCACGAGGGCAAGGCCTA
CTTCCCACGCGAGGGCGTGTTTCGTGTTCAACGGC

SEQ ID NO: 20

SARs Spike glycoprotein Fragment I protein sequence without the N-linked glycosylation sites (807 amino acids encoded by SEQ ID NO: 19):

AVDCSQNPLAELKCSVKSF EIDKGIYQTSNFRVVP SGDVRFNPNIANLCPFG EVFAATKFPSVYA
WERKKISNCVADYSVLYNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGV
IADYNYKL PDDFMGCVLAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVFPSPDGKPCPTP
PALNCYWPLNDYG FYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTD LIKNQCVNFNFNGLTG
TGVLT PSSSRFQPFQFGRDVSDFDTSVRDPKTSEILDISPCSFGGVSVITPGTNAASEVAVLYQ
DVACTDVSTAIHADQLTPAWRIYSTGNVVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSL
RSTSQKSIVAYTMSLGADSSIAYSANTIAIPTNFAISITTEVMPVSMAKTSVDCNMYICGDSTECANL
LLQYGSFCTQLNRALSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDLPKPTKRSFI
EDLLFNKVTLADAGFMKQYGECLGDINARDLICAQKFNGLTVL PPLLDDMIAAYTAALVSGTATA
GWTFGAGAAALQIPFAMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQ
DVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAA
EIRASANLAATKMS ECVLGQSKRVD FCGKGYHLSFPQAAPHGVVFLHVTYVPSQERNFATAPAI
CHEGKAYFPREGV FVFNG

SEQ ID NO: 21: SARs Spike glycoprotein Fragment II synthetic DNA sequence with N-linked glycosylation site mutations (744bps):

GTGCTGTACAAC TCCGCCTTCTTCTCCACCTTCAAGTGCTACGGCGTGTC
CGCCACCAAGCTGAACGACCTGTGCTTCTCCAACGTGTACGCCGACTCCT
TCGTGGTGAAGGGCGACGACGTGCGCCAGATCGCCCCAGGCCAGACCGG
CGTGATCGCCGACTACAAC TACAAGCTGCCAGACGACTTCATGGGCTGC
GTGCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCAACT
ACAAC TACAAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCCATTCGA
GCGCGACATCTCCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCACC
CCACCAGCCCTGAACTGCTACTGGCCACTGAACGACTACGGCTTCTACAC
CACCACCGGCATCGGCTACCAGCCATAACCGCGTGGTGGTGTCTCCTTC
GAGCTGCTGAACGCCCCAGCCACCGTGTGCGGCCCAAAGCTGTCCACCG
ACCTGATCAAGAACCAGTGCGTGAAC TTCAACTTCAACGGCCTGACCGGC
ACCGGCGTGCTGACCCCATCCTCCAAGCGCTTCCAGCCATTCCAGCAGTT
CGGCCGCGACGTGTCCGACTTCACCGACTCCGTGCGCGACCCAAAGACC
TCCGAGATCCTGGACATCTCCCCATGCTCCTTCGGCGGGCGTGTCGTGAT
CACCCAGGCACCAACGCCGCCTCCGAGGTGGCCGTGCTGTACCAGGAC
GTG

SEQ ID NO: 22: SARs Spike glycoprotein Fragment II protein sequence without the N-linked glycosylation sites (248 amino acids, encoded by SEQ ID 21):

VLYNSAFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKL PDDFMG
CVLAWNTRNIDATSTGNYNKYRYLRHGKLRPFERDISNVFPSPDGKPCPTPALNCYWPLNDYG
FYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTD LIKNQCVNFNFNGLTGTGVLT PSSSRFQPF
QQFGRDVSDFDTSVRDPKTSEILDISPCSFGGVSVITPGTNAASEVAVLYQDV

SEQ ID NO: 23: SARS Spike glycoprotein Fragment III synthetic DNA sequence with N-linked glycosylation site mutations (834 bps):

GCCGAGCAGGACCGCAACACCCGCGAGGTGTTTCGCCCAGGTGAAGCAGA
TGTACAAGACCCCAACCCTGAAGTACTTCGGCGGCTTCAACTTCGCCCAG
ATCCTGCCAGACCCACTGAAGCCAACCAAGCGCTCCTTCATCGAGGACCT
GCTGTTCAACAAGGTGACCTTGGCCGACGCCGGCTTCATGAAGCAGTAC
GGCGAGTGCTTGGGCGACATCAACGCCCGCGACCTGATCTGCGCCCAGA
AGTTCAACGGCCTGACCGTGCTGCCACCACTGCTGACCGACGACATGAT

CGCCGCCTACACCGCCGCCCTGGTGTCCGGCACCGCCACCGCCGGCTGG
ACCTTCGGGCGCCGGCGCCGCCCTGCAGATCCCATTTCGCCATGCAGATGG
CCTACCGCTTCAACGGCATCGGCGTGACCCAGAACGTGCTGTACGAGAA
CCAGAAGCAGATCGCCAACCAGTTCAACAAGGCCATCTCCCAGATCCAG
GAGTCCCTGACCACCACCTCCACCGCCCTGGGCAAGCTGCAGGACGTGG
TGAACCAGAACGCCAGGGCCCTGAACACCCTGGTGAAGCAGCTGTCCTC
CAACTTCGGCGCCATCTCCTCCGTGCTGAACGACATCCTGTCCCGCCTGG
ACAAGGTGGAGGCCGAGGTGCAGATCGACCGCCTGATCACCGGCCGCCCT
GCAGTCCCTGCAGACCTACGTGACCCAGCAGCTGATCCGCGCCGCCGAG
ATCCGCGCCTCCGCCAACCTGGCCGCCACCAAGATGTCCGAGTGCCTGC
TGGGCCAGTCCAAGCGCGTGGACTTCTGCGGCAAGGGCTACCACCTG

SEQ ID NO: 24: SARs Spike glycoprotein Fragment III protein sequence without the N-linked glycosylation sites (278 amino acids, encoded by SEQ ID NO: 23):

AEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDPLKPTKRSFIEDLLFNKVTADAGFMKQ
YGECLGDINARDLICAQKFNGLTVPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPFAMQ
MAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLVKQLS
SNFGAISSVLNDILSRDLKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSECVLG
QSKRVDFCGKGYHL

SEQ ID NO: 25: SARs Spike glycoprotein Fragment IV synthetic DNA sequence with N-linked glycosylation site mutations (2034 bps):

GTGCTGTAACTCCGCCCTTCTTCTCCACCTTCAAGTGCTACGGCGTGTCGCCACCAAGCT
GAACGACCTGTGCTTCTCCAACGTGTACGCCGACTCCTTCGTGGTGAAGGGCGACGACGTG
CGCCAGATCGCCCCAGGCCAGACCGGCGTGATCGCCGACTACAACTACAAGCTGCCAGAC
GACTTCATGGGCTGCGTGCTGGCCTGGAACACCCGCAACATCGACGCCACCTCCACCGGCA
ACTACAACCTACAAGTACCGCTACCTGCGCCACGGCAAGCTGCGCCATTTCGAGCGCGACAT
CTCCAACGTGCCATTCTCCCCAGACGGCAAGCCATGCACCCACCAAGCCCTGAACTGCTAC
TGGCCACTGAACGACTACGGCTTCTACACCACCACCGGCATCGGCTACCAGCCAAAGCTGTC
TGGTGGTGCTGTCTTCGAGCTGCTGAACGCCCCAGCCACCGTGTCGCGGCCAAAGCTGTC
CACCGACCTGATCAAGAACCAGTGCGTGAACCTTCAACTTCAACGGCCTGACCGGCACCGGC
GTGCTGACCCCATCTCCAAGCGCTTCCAGCCATTCCAGCAGTTTCGGCCGCGACGTGTCCG
ACTTCACCGACTCCGTGCGCGACCCAAAGACCTCCGAGATCCTGGACATCTCCCCATGCTC
CTTCGGCGGCGTGTCGGTGATCACCCAGGCACCAACGCCGCCCTCCGAGGTGGCCGTGCT
GTACCAAGGACGTGGCCTGCACCGACGTGTCCACCGCCATCCACGCCGACCAAGCTGACCCC
AGCCTGGCGCATCTACTCCACCGGCAACAAGTGTTCCAGACCCAGGCGGGCTGCCTGATC
GGCGCCGAGCAGTGACACCTCTACAGTGCGACATCCCAATCGGCGCCGGCATCTGC
GCCTCTACCAACCGTGTCCTGCTGCGCTCCACCTCCAGAAAGTCCATCGTGGCC TACA
CCATGTCCCTGGGCGCCGACTCCTCCATCGCCTACTCCGCCAACACCATCGCCATCCCAAC
CAACTTCGCCATCTCCATCACCAACGAGGTGATGCCAGTGTCATGGCCAAGACCTCCGTG
GACTGCAACATGTACATCTGCGGCGACTCCACCGAGTGCGCCAACCTGCTGCTGCAGTACG
GCTCCTTCTGCACCCAGCTGAACCGCGCCCTGTCCGGCATCGCCGCCGAGCAGGACCGCA
ACACCCGCGAGGTGTTCCGCCAGGTGAAGCAGATGTACAAGACCCCAACCCTGAAGTACTT
CGGCGGCTTCAACTTCGCCAGATCCTGCCAGACCCACTGAAGCCAACCAAGCGCTCCTTC
ATCGAGGACCTGCTGTTCAACAAGGTGACCCTGGCCGACGCGCGCTTCATGAAGCAGTACG
GCGAGTGCTGGGCGACATCAACGCCCGCGACCTGATCTGCGCCAGAAAGTTCAACGGCC
TGACCGTGCTGCCACCACTGCTGACCGACGACATGATCGCCGCCCTACACCGCCGCCCTGGT
GTCCGGCACCGCCACCGCCGGCTGGACCTTCGGCGCCGGCGCCGCCCTGCAGATCCCAT
CGCCATGCAGATGGCCTACCGCTTCAACGGCATCGGCGTGACCCAGAACGTGCTGTACGAG
AACCAGAAGCAGATCGCCAACCAGTTCAACAAGGCCATCTCCAGATCCAGGAGTCCCTGA
CCACCACCTCCACCGCCCTGGGCAAGCTGCAGGACGTGGTGAACCAGAACGCCAGGCC
TGAACACCCTGGTGAAGCAGCTGTCTCCAACCTTCGGCGCCATCTCCTCCGTGCTGAACGA
CATCCTGTCCCGCCTGGACAAGGTGGAGGCCGAGGTGCAGATCGACCGCCTGATCACCGG
CCGCTGCAGTCCCTGCAGACCTACGTGACCCAGCAGCTGATCCGCGCCGCCGAGATCCG
CGCCTCCGCCAACCTGGCCGCCACCAAGATGTCCGAGTGCGTGCTGGGCCAGTCCAAGCG
CGTGGACTTCTGCGGCAAGGGCTACCACCTG

SEQ ID NO: 26: SARs Spike glycoprotein Fragment IV protein sequence without the N-linked glycosylation sites (678 amino acids, encoded by SEQ ID NO: 25):

VLYNSAFFSTFKCYGVSATKLNLCFSNVYADSFVVKGDDVRQIAPGQTGVIADYNYKLPDDFMG
CVLAWNTRNIDATSTGNVNYKYRYLRHGKLRPFERDISNVPFSPDGKPCTPPALNCYWPLNDYG
FYTTTGIGYQPYRVVLSFELLNAPATVCGPKLSTDLIKNQCVNFNFNGLTGTGVLTPSSKRFQPF
QQFGRDVSDFTDSVRDPKTSEILDSPCSFGGVSVITPGTNAASEVAVLYQDVACTDVSTAIHADQ
LTPAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASYHTVSLRSTSQKSIVAYTMSL
GADSSIAYSANTIAIPTNFASITTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRA
LSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFAQILPDPLKPTKRSFIEDLLFNKVTLADAG
FMKQYGECLGDINARDLICAQKFNGLTVLPPLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPF
AMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTSTALGKLQDVVNQNAQALNTLV
KQLSSNFGAISSVLNDILSRDKVEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMSE
CVLGQSKRVDFCGKGYHL